Amendment to the Claims:

This listing of claims will replace all prior versions, and listings, of claims in the application:

1. **(Currently Amended)** A mutant mammalian G protein-coupled receptor having an amino acid sequence which differs from a wild type G protein-coupled receptor having a wild type amino acid sequence comprising an amino acid motif ($X_1X_2X_3X_4$) closer to the C-terminal end than the N-terminal end of said wild type amino acid sequence, wherein the wild-type receptor is selected from the group consisting of the chemokine α family of receptors and wherein:

X_1 denotes an amino acid residue at position 1 of said motif and is selected from the group consisting of Phe, Leu, Val, and Tyr;

X_2 denotes an amino acid residue at position 2 of said motif and is selected from the group consisting of Phe, Lys and Gln;

X_3 denotes an amino acid residue at position 3 of said motif and is selected from the group consisting of Leu, Arg, Glu, Asn, Gln, Ser, Ala, Leu ; and

X_4 denotes an amino acid residue at position 4 of said motif and is selected from the group consisting of Ala, Cys, Asp, Glu, Gly, Ser, Thr and Tyr; and

wherein said mutant receptor comprises a seventh transmembrane domain with a carboxy terminal end;

at least one point mutation at a position in said amino acid motif;

wherein upon interaction with a ligand to modulate a signal transduction pathway in a cell, a signal generated by said mutant receptor is greater than a signal generated upon interaction of said ligand with a wild type G protein-coupled receptor.

2. **(Original)** The receptor of claim 1, wherein said cell is a yeast cell.

3. **(Original)** The receptor of claim 2, wherein said receptor acts as a surrogate for an endogenous yeast pheromone receptor in a pheromone response pathway of said cell.

4. **(Original)** The receptor of claim 2, wherein said cell belongs to the species *Saccharomyces cerevisiae*.

5. **(Original)** The receptor of claim 1, wherein said cell is a mammalian cell.

6. **(Original)** The receptor of claim 1, wherein said receptor containing said amino acid motif with no point mutation thereon generates no detectable signal.

7. **(Original)** The receptor of claim 1, wherein said point mutation comprises mutagenization at position 4 of said amino acid motif to Arg or to Lys.

8. **(Currently Amended)** The receptor of claim 1, wherein said wild type G protein-coupled receptor is IL8A receptor.

9. **(Original)** The receptor of claim 8, wherein said point mutation is selected from the group consisting of : Arg to Trp at position 73, Met to Ile at position 246; and Gly to Arg at position 320.

10. **(Original)** The receptor of claim 8, wherein said ligand is interleukin 8 (IL8) or melanoma growth-stimulating activity-alpha (MGSA/GROα).

11. **(Currently Amended)** The receptor of claim 1, wherein said wild type G protein-coupled receptor is a human receptor.

12. **(Cancelled)**

13. **(Cancelled)**

14. **(Currently Amended)** The receptor of claim ~~13~~52, comprising an amino acid sequence LAYSNSSVNPIIYAFLSEN(FRKR)YKQV (SEQ ID NO:1) wherein said mutant amino acid motif within said sequence is (FRKR) (SEQ ID NO:2).

Claims 15-42. **(Cancelled)**

43. **(Previously Presented)** The receptor of claim 1, wherein said wild type G protein coupled receptor is a member of the rhodopsin family of receptors.

44. **(Previously Presented)** A mutant mammalian IL8A receptor having an amino acid sequence which differs from a wild type IL8A receptor having a wild type amino acid sequence comprising an amino acid motif ($X_1X_2X_3X_4$) proximal to the carboxy terminal end of said wild type amino acid sequence, wherein:

X_1 denotes an amino acid residue at position 1 of said motif and is selected from the group consisting of Phe, Leu, Val, and Tyr;

X_2 denotes an amino acid residue at position 2 of said motif and is selected from the group consisting of Phe, Lys and Gln;

X_3 denotes an amino acid residue at position 3 of said motif and is selected from the group consisting of Leu, Arg, Glu, Asn, Gln, Ser, Ala, Leu ; and

X_4 denotes an amino acid residue at position 4 of said motif and is selected from the group consisting of Ala, Cys, Asp, Glu, Gly, Ser, Thr and Tyr; and

wherein said mutant receptor comprises a seventh transmembrane domain with a carboxy terminal end; and

at least one point mutation at a position in said amino acid motif, wherein said point mutation is selected from the group consisting of: Arg to Trp at position 73, Met to Ile at position 246, and Gly to Arg at position 320, wherein upon interaction with a ligand to modulate a signal transduction pathway in a cell, a signal generated by said mutant receptor is greater than a signal generated upon interaction of said ligand with a wild type IL8A receptor.

45. **(Previously Presented)** The receptor of claim 44, wherein said cell is a yeast cell.

46. **(Previously Presented)** The receptor of claim 45, wherein said receptor acts as a surrogate for an endogenous yeast pheromone receptor in a pheromone response pathway of said cell.

47. **(Previously Presented)** The receptor of claim 45, wherein said cell belongs to the species *Saccharomyces cerevisiae*.

48. **(Previously Presented)** The receptor of claim 44, wherein said cell is a mammalian cell.

49. **(Previously Presented)** The receptor of claim 44, wherein said receptor containing said amino acid motif with no point mutation therein generates no detectable signal.

50. **(Previously Presented)** The receptor of claim 44, wherein said point mutation comprises mutagenization at position 4 of said amino acid motif to Arg or to Lys.

51. **(Previously Presented)** The receptor of claim 44, wherein said ligand is interleukin 8 (IL8) or melanoma growth-stimulating activity-alpha (MGSA/GROα).

52. **(Previously Presented)** A mutant galanin receptor-1 having an amino acid sequence which differs from a wild type galanin receptor-1 having a wild type amino acid sequence comprising an amino acid motif ($X_1X_2X_3X_4$) proximal to the carboxy terminal end of said wild type amino acid sequence, wherein:

X_1 denotes an amino acid residue at position 1 of said motif and is selected from the group consisting of Phe, Leu, Val, and Tyr;

X_2 denotes an amino acid residue at position 2 of said motif and is selected from the group consisting of Phe, Lys and Gln;

X_3 denotes an amino acid residue at position 3 of said motif and is selected from the group consisting of Leu, Arg, Glu, Asn, Gln, Ser, Ala, Leu ; and

X_4 denotes an amino acid residue at position 4 of said motif and is selected from the group consisting of Ala, Cys, Asp, Glu, Gly, Ser, Thr and Tyr; and

wherein said mutant receptor comprises a seventh transmembrane domain with a carboxy terminal end; and

at least one point mutation in said amino acid motif comprising Gly to Ala at position 320, wherein upon interaction with a ligand to modulate a signal transduction pathway in a cell, a signal generated by said mutant receptor is greater than a signal generated upon interaction of said ligand with a wild type galanin receptor-1.

53. **(Previously Presented)** The amino acid motif of claim 52, wherein X_1 denotes an amino acid residue at position 1 of said motif and is Phe;

X_2 denotes an amino acid residue at position 2 of said motif and is selected from the group consisting of Arg;

X_3 denotes an amino acid residue at position 3 of said motif and is selected from the group consisting of Lys; and

X_4 denotes an amino acid residue at position 4 of said motif and is Ala, Cys, Asp, Glu, Gly, Ser, Thr and Tyr.

54. **(Previously Presented)** The receptor of claim 52 or 53, wherein said cell is a yeast cell.

55. **(Previously Presented)** The receptor of claim 54, wherein said receptor acts as a surrogate for an endogenous yeast pheromone receptor in a pheromone response pathway of said cell.

56. **(Previously Presented)** The receptor of claim 54, wherein said cell belongs to the species *Saccharomyces cerevisiae*.

57. **(Previously Presented)** The receptor of claim 52 or 53, wherein said cell is a mammalian cell.

58. **(Previously Presented)** The receptor of claim 52 or 53, wherein said receptor containing said amino acid motif with no point mutation therein generates no detectable signal.

59. **(Previously Presented)** The receptor of claim 52 or 53, wherein said receptor comprises mutagenization at position 4 of said amino acid motif to Arg or to Lys.

60. **(Cancelled)**

61. **(Previously Presented)** The mutant mammalian G protein-coupled receptor of claim 1, wherein said amino acid motif commences 5-10 acid residues from the carboxy terminal end of said wild type amino acid sequence.

62. **(Previously Presented)** The mutant mammalian G protein-coupled receptor of claim 44, wherein said amino acid motif commences 5-10 acid residues from the carboxy terminal end of said wild type amino acid sequence.

63. **(Previously Presented)** The mutant mammalian G protein-coupled receptor of claim 52, wherein said amino acid motif commences 5-10 acid residues from the carboxy terminal end of said wild type amino acid sequence.

64. **(Cancelled)**

65. **(Cancelled)**

66. **(Cancelled)**

67. **(New)** The receptor of claim 44, comprising an amino acid sequence LGFLHSCLNPIIYAFIGQN[FRNG]FLKM (SEQ ID NO:3) wherein said mutant amino acid motif within said sequence is (FRKG) (SEQ ID NO:4).

68. **(New)** The receptor of claim 1, wherein the chemokine α receptor is selected from the group consisting of receptors for IL-8, melanoma growth-stimulating activity (MGSA/GRO), platelet factor 4 (PF-4), β thromboglobulin (βTG), IP-10, and ENA-78.